



REPLACEMENT SHEET
Application No. 10/506,406, filed 3/14/05
Inventors: Swiercz et al.

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	GAATTCTGCAGCTCAGCAGCCGCCAGAGCAGGACGAACCGCCAATCGCAAGGCACC	
1	-----+-----+-----+-----+-----+-----+-----+-----+ 60	
	CTTAAGGACGTCGAGTCGTGGCGGGTCTCGTCTGCTTGGCGGTTAGCGTTCCGTGG	
	TCTGAGAACCTCAGGATGCAGATGTCTCCAGCCCTCACCTGCCTAGTCCTGGGCCCTGGCC	
61	-----+-----+-----+-----+-----+-----+-----+-----+ 120	
	AGACTCTTGAAGTCCTACGTCTACAGAGGTCGGAGTGGACGGATCAGGACCCGGACCGG	
aa	M Q M S P A L T C L V L G L A - Signal Peptide	
	CTTGTCTTGGTGAAGGGTCTGCTGTGCACCATCCCCATCCTACGTGGCCCACCTGGCC	
121	-----+-----+-----+-----+-----+-----+-----+-----+ 180	
	GAACAGAAACCACTTCCCAGACGACACGTGGTAGGGGGTAGGATGCACCGGGTGGACCGG	
aa	L V F G E G S A V H H P P S Y V A H L A 12 Start Mature Protein	
	TCAGACTTCGGGGTGAGGGTGTTCAGCAGGTGGCGCAGGCCTCCAAGGACCGAACGTG	
181	-----+-----+-----+-----+-----+-----+-----+-----+ 240	
	AGTCTGAAGCCCCACTCCCACAAAGTCGTCCACCGCGTCCGGAGGTTCTGGCGTTGCAC	
aa	S D F G V R V F Q Q V A Q A S K D R N V 32	
	GTTTCTCACCTATGGGGTGGCCTCGGTGTTGGCCATGCTCCAGCTGACAACAGGAGGA	
241	-----+-----+-----+-----+-----+-----+-----+-----+ 300	
	CAAAGAGTGGGATAACCCACCGGAGGCCAACACCGGTACGAGGTCGACTGTTGTCCTCCT	
aa	V F S P Y G V A S V L A M L Q L T T G G 52	
	GAAACCCAGCAGCAGATTCAAGCAGCTATGGGATTCAAGATTGATGACAAGGGCATGGCC	
301	-----+-----+-----+-----+-----+-----+-----+-----+ 360	
	CTTTGGGTCGTCGTCAAGTTCGTGATACCTAAGTTCTAACTACTGTTCCCGTACCGG	
aa	E T Q Q Q I Q A A M G F K I D D K G M A 72	
	CCCGCCCTCCGGCATCTGTACAAGGAGCTATGGGCCATGGAACAAGGATGAGATCAGC	
361	-----+-----+-----+-----+-----+-----+-----+-----+ 420	
	GGGCGGGAGGCCGTAGACATGTTCCCTCGAGTACCCCGGTACCTGTTCTACTCTAGTCG	
aa	P A L R H L Y K E L M G P W N K D E I S 92	
	ACCACAGACGCGATCTCGTCCAGCGGGATCTGAAGCTGGTCCAGGGCTTCATGCCAAC	
421	-----+-----+-----+-----+-----+-----+-----+-----+ 480	
	TGGTGTCTCGCCTAGAAGCAGGTGCCCTAGACTTCGACCAAGGTCCCGAAGTACGGGGTG	
aa	T T D A I F V Q R D L K L V Q G F M P H 112	
	TTCTTCAGGCTGTTCCGGAGCACGGTCAAGCAAGTGGACTTTCAAGAGGTGGAGAGGCC	
481	-----+-----+-----+-----+-----+-----+-----+-----+ 540	
	AAGAAGTCCGACAAGGCCCTCGTGCCAGTTGTTCACCTGAAAAGTCTCCACCTCTCGG	
aa	F F R L F R S T V K Q V D F S E V E R A 132	

FIG.1A

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AGATTCATCATCAATGACTGGGTGAAGACACACACAAAAGGTATGATCAGCAACTTGCTT
541+.....+.....+.....+.....+.....+.....+.....+ 600
aa TCTAAGTAGTAGTTACTGACCCACTTCTGTGTGTTTCATACTAGTCGTTGAACGAA
R F I I N D W V K T H T K G M I S N L L 152

GGGAAAGGAGCCGTGGACCAGCTGACACGGCTGGTGTGGTAATGCCCTACTTCAAC
601+.....+.....+.....+.....+.....+.....+.....+ 660
aa CCCTTCCTCGGCACCTGGTCACTGTGCGGACACGACCACTTACGGGAGATGAAGTTG
G K G A V D Q L T R L V L V N A L Y F N 172

GGCCAGTGGAAAGACTCCCTCCCCGACTCCAGCACCCACCGCCGCCTTCCACAAATCA
661+.....+.....+.....+.....+.....+.....+.....+ 720
aa CCGGTACCTCTGAGGGAAAGGGGCTGAGGTGCGTGGTGGCGGGAGAAGGTGTTAGT
G Q W K T P F P D S S T H R R L F H K S 192

GACGGCAGCACTGTCTCTGTGCCATGATGGCTCAGACCAACAAGTTCAACTATACTGAG
721+.....+.....+.....+.....+.....+.....+.....+ 780
aa CTGCCGTCGTGACAGAGACACGGGTACTACCGAGTCTGGTTGTTCAAGTTGATATGACTC
D G S T V S V P M M A Q T N K F N Y T E 212

TTCACCACGCCGATGCCATTACTACGACATCCTGGAACGCCCTACACGGGACACC
781+.....+.....+.....+.....+.....+.....+.....+ 840
aa AAGTGGTGCAGGGCTACCGGTAAATGATGCTGAGGACCTTGACGGGATGGTGCCTGTGG
F T T P D G H Y Y D I L E L P Y H G D T 232

CTCAGCATGTTATTGCTGCCCTTATGAAAAAGAGGTGCCCTCTGCCCTACCAAC
841+.....+.....+.....+.....+.....+.....+.....+ 900
aa GAGTCGTACAAGTAACGACGGGAATACTTTCTCCACGGAGAGAGACGGGAGTGGTTG
L S M F I A A P Y E K E V P L S A L T N 252

ATTCTGAGTGCCAGCTCATGCCACTGGAAAGGAAACATGACCAAGGCTGCCCGCCTC
901+.....+.....+.....+.....+.....+.....+.....+ 960
aa TAAGACTCACGGGTCGAGTAGTCGGTACCTTCCGGTTACTGGTCCGACGGGGCGGAG
I L S A Q L I S H W K G N M T R L P R L 272

CTGGTTCTGCCCAAGTTCTCCCTGGAGACTGAAGTCGACCTCAGGAAGCCCCTAGAGAAC
961+.....+.....+.....+.....+.....+.....+.....+ 1020
aa GACCAAGACGGGTTCAAGAGGGACCTCTGACTTCAGCTGGAGTCCTCGGGGATCTCTTG
L V L P K F S L E T E V D L R K P L E N 292

CTGGGAATGACCGACATGTTCAGACAGTTCAGGCTGACTTCACGAGTCTTCAGACCAA
1021+.....+.....+.....+.....+.....+.....+.....+ 1080
aa GACCCTTACTGGCTGTACAAGTCTGTCAGGACTGAAGTGCTCAGAAAGTCTGGTT
L G M T D M F R Q F Q A D F T S L S D Q 312

FIG. 1B

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GAGCCTCTCACGTCGCAGCGCTGCAGAAAGTGAAGATCGAGGTGAACGAGAGTGGC
1081+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1140
CTCGGAGAGGTGCAGCGCGTCCGCACGTCTTCACTTCTAGCTCCACTTGCTCTCACCG
aa E P L H V A Q A L Q K V K I E V N E S G 332

ACGGTGGCCTCCTCATCCACAGCTGTCAAGTCTCAGCCGCATGGCCCCGAGGAGATC
1141+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1200
TGCCACCGGAGGAGTAGGTGTCGACAGTATCAGAGTCGGCGTACCGGGGGCTCTCTAG
aa T V A S S S T A V I V S A R M A P E E I 352

ATCATGGACAGACCCTCCTCTTGTGGTCCGGCACAAACCCCACAGGAACAGTCCTTTTC
1201+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1260
TAGTACCTGTCTGGGAAGGAGAACACCAGGCCGTGTTGGGTGTCCTGTCAAGGAAAAG
aa I M D R P F L F V V R H N P T G T V L F 352

ATGGGCCAAGTGAATGGAACCCCTGACCCCTGGGAAAGACGCCCTCATCTGGACAAAATG
1261+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1320
TACCCGGTTCACTACCTTGGGACTGGGACCCCTTCTGCGGAAGTAGACCCCTGTTTGAC
aa M G Q V M E P * 379

GAGATGCATGGAAAGAAGAAACTCCGAAGAAAAGAATTAGTGTAAATGACTCTTC
1321+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1380
CTCTACGTAGCCCTTCTTCTTGTAGGGCTCTTCTTAAATCACAATTACTGAGAAAG

TGAAGGAAGAGAACATTGCCTTTGTTAAAAGATGGTAAACCAGATCTGTCTCCAAG
1381+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1440
ACTTCCTTCTTCTGTAAACGGAAAACAATTCTACCATTTGGTCTAGACAGAGGTTC

ACCTTGGCCTCCCTGGAGGACCTTAGGTCAAACCTCCCTAGTCTCCACCTGAGACCCCT
1441+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1500
TGGAACCGGAGAGGAACCTCCTGGAAATCCAGTTGAGGGATCAGAGGTGGACTCTGGGA

GGGAGAGAACGTTGAAGCACAACCTCCCTAACGGTCTCCAAACCAAGACGGTGACGCCCTGCG
1501+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1560
CCCTCTTCAAACCTCGTGTGAGGGAAATCCAGAGGTGGTCTGCCACTGCGGACGC

GGACCATCTGGGGCACCTGCTTCCACCCGCTCTCTGCCACTCGGGCTGCAGACCTGG
1561+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1620
CCTGGTAGACCCCGTGGACGAAGGTGGCAGAGAGACGGGTGAGCCAGACGTCTGGACC

TTCCCACTGAGGCCCTTGCAGGATGGAACATCAGGGCTTACAGGAGCTTGTGTGCCT
1621+.....+.....+.....+.....+.....+.....+.....+.....+.....+ 1680
AAGGGTGACTCCGGAAACGTCCACCTGATGCCCGAATGTCCCTGAAAACACACGGA

FIG. 1C

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1681 GGTAGAAACTATTTCTGTTCCAGTCACATTGCCATCACTCTTGTACTGCCTGCCACCGCG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1740
CCATCTTGATAAAGACAAGGTCAGTGTACGGTAGTGAGAACATGACGGACGGTGGCGC

1741 GAGGAGGCTGGTGACAGGCCAAAGGCCAGTGGAAAGAACACCCCTTCATCTCAGAGTCCA
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 1800
CTCCTCCGACCCTGTCCGGTTCCGGTCACCTTCTTGTGGGAAAGTAGAGTCTCAGGT

1801 CTGTGGCACTGGCCACCCCTCCCCAGTACAGGGGTGCTGCAGGTGGCAGAGTGAATGTCC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 1860
GACACCGTGACCGGTGGGGAGGGGTATGTCCCCACGACGTCCACCGTCTCACTTACAGG

1861 CCCATCATGTGGCCAACTCTCCTGGCCTGGCATCTCCCTCCCCAGAAACAGTGTGCAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 1920
GGGTAGTACACCGGGTTGAGAGGACCGGACCGTAGAGGGAGGGGTCTTGTACACGTA

1921 GGGTTATTTGGAGTGTAGGTGACTTGTAACTCATTGAAGCAGATTCTGCTTCTTTT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 1980
CCCAATAAAACCTCACATCCACTGAACAAATGAGTAACCTCGTCTAAAGACGAAGGAAAA

1981 ATTTTATAGGAATAGAGGAAGAAATGTCAGATGCGTGCCCAGCTCTCACCCCCCAATC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2040
TAAAAAATATCCTTATCTCCTTCTTACAGTCTACGCACGGTCGAGAAGTGGGGGGTTAG

2041 TCTTGGTGGGGAGGGGTGTACCTAAATATTATCATATCCTGCCCTTGAGTGCTTGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2100
AGAACCCACCCCTCCCCACATGGATTATAAATAGTATAGGAACGGGAACTCACGAACAAAT

2101 GAGAGAAAGAGAACTACTAAGGAAAATAATATTATTAAACTCGCTCTAGTGTTC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2160
CTCTCTTCTCTGATGATTCTTATTATAATAAAATTGAGCGAGGATCACAAAGAAA

2161 GTGGTCTGTGTACCGTATCTCAGGAAGTCCAGCCACTTGACTGGCACACACCCCTCCGG
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2220
CACCAGACACAGTGGCATAGAGTCCTCAGGTCGGTGAACGTACCGTGTGGGAGGCC

2221 ACATCCAGCGTGACGGAGCCCACACTGCCACCTTGTGGCCGCTGAGACCCCTCGCGCCCC
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2280
TGTAGGTCGCACTGCCTCGGGTGTGACGGTGGAACACCGGCGGACTCTGGGAGCGCGGGG

2281 CCGCGCCCCCGCGCCCCCTTTTCCCTTGATGGAAATTGACCATACAATTCTACCT
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ + 2340
GGCGCGGGGGGGCGCGGGGAGAAAAAGGGGAACACCTTAACTGGTATGTTAAAGTAGGA

FIG. 1D

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CCTTCAGGGGATCAAAAGGACGGAGTGGGGGGACAGAGACTCAGATGAGGACAGAGTGTT
2341 -----+-----+-----+-----+-----+-----+-----+-----+ 2400
GGAAGTCCCCTAGTTTCTGCCTCACCCCCCTGTCTTGAGTCTACTCCTGTCTCACCA

TTCCAATGTGTTCAATAGATTAGGAGCAGAAATGCAAGGGGCTGCATGACCTACCAGGA
2401 -----+-----+-----+-----+-----+-----+-----+-----+ 2460
AAGGTTACACAAGTTATCTAAATCCTCGTCTTACGTTCCCGACGTACTGGATGGTCT

CAGAACCTTCCCCAATTACAGGGTGAUTCACAGCCGCATTGGTGAUTCACTCAATGTGT
2461 -----+-----+-----+-----+-----+-----+-----+-----+ 2520
GTCTTGAAGGGGTTAATGTCCCACTGAGTGTGGCGTAACCACTGAGTGAAGTTACACA

CATTTCCGGCTGCTGTGTGAGCAGTGGACACGTGAGGGGGGGGGTGGGTGAGAGAGACA
2521 -----+-----+-----+-----+-----+-----+-----+-----+ 2580
GTAAAGGCCGACGACACACACTCGTCACCTGTGCACTCCCCCCCCACCCACTCTCTGT

GGCAGCTCGGATTCAACTACCTTAGATAATATTCTGAAAACCTACCAGCCAGAGGTAG
2581 -----+-----+-----+-----+-----+-----+-----+-----+ 2640
CCGTCGAGCCTAACGGATGGAATCTATTATAAAGACTTTGGATGGTCGGTCTCCCATC

GGCACAAAGATGGATGTAATGCACTTGGGAGGCCAAGGCCGGAGGATTGCTTGAGCCA
2641 -----+-----+-----+-----+-----+-----+-----+-----+ 2700
CCGTGTTCTACCTACATTACGTGAAACCCCTCCGGTCCGCCCTCTAACGAACTCGGGT

GGAGTTCAAGACCAGCCTGGCAACATACCAAGACCCCCGTCTCTTAAAAATATATA
2701 -----+-----+-----+-----+-----+-----+-----+-----+ 2760
CCTCAAGTTCTGGTCGGACCCGTTGTATGGTTCTGGGGCAGAGAAATTATATATAT

TTTTAAATATACTAAATATATATTCTAATATCTTTAAATATATATATATATTTAAAG
2761 -----+-----+-----+-----+-----+-----+-----+-----+ 2820
AAAATTATATGAATTATATAAAGATTAGAAATTATATATATATATAAAAATTTC

ACCAATTATGGGAGAATTGCACACAGATGTGAAATGAATGTAATCTAACAGAC
2821 -----+-----+-----+-----+-----+-----+-----+-----+ 2876
TGGTTAAATACCCCTTTAACGTGTCTACACTTTACTACATTAGATTATCTCG

FIG. 1E

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MQMSPALTCVLGLALVFGEGLA
Signal Peptide

VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST
VKQVDFSEVERARFIINDWKTKGMISNLLKGAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRLFHKS DGSTSVSPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAP
YEKEVPLSALTNIQLSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIIMDRPFLF
VVRHNPTGTVLFMGQVMEP

FIG. 2A

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10 20 30 40 50 60
| | | | | |
VHHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQA

70 80 90 100 110 120
| | | | | |
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST

130 140 150 160 170 180
| | | | | |
VKQVDFSEVERARFIINDWVKHTKGMSNLLKGAVDQLTRLVLVNALYFNGQWKTPFP

190 200 210 220 230 240
| | | | | |
DSSTHRRLFHKS DGSTVSVP MMAQTNKFNYTEFTT PDGHYYDILELPYHGDTLSMFIAAP

250 260 270 280 290 300
| | | | | |
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR

310 320 330 340 350 360
| | | | | |
QFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVASSSTAVIVSARMAPEEIIMDRPFLF

370
|
VVRHNPTGTVLFMGQVMEP

FIG.2B

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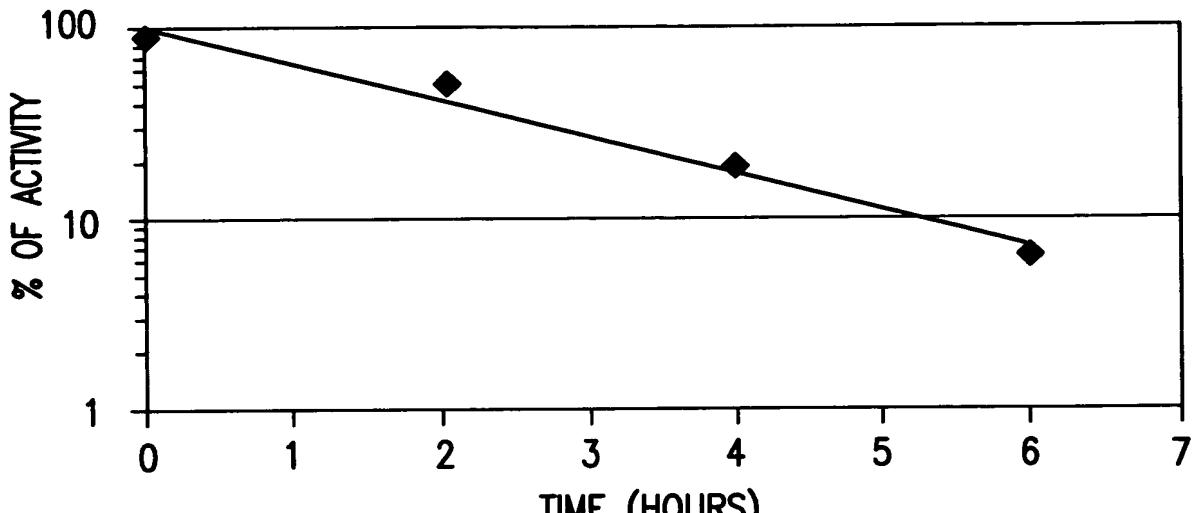


FIG.3

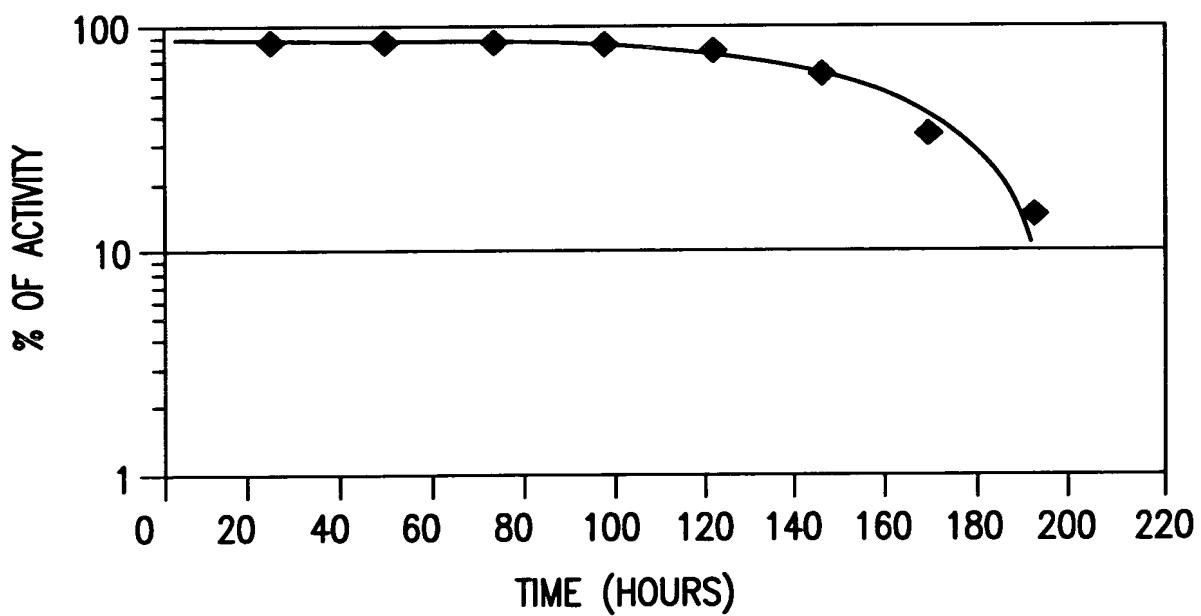


FIG.4

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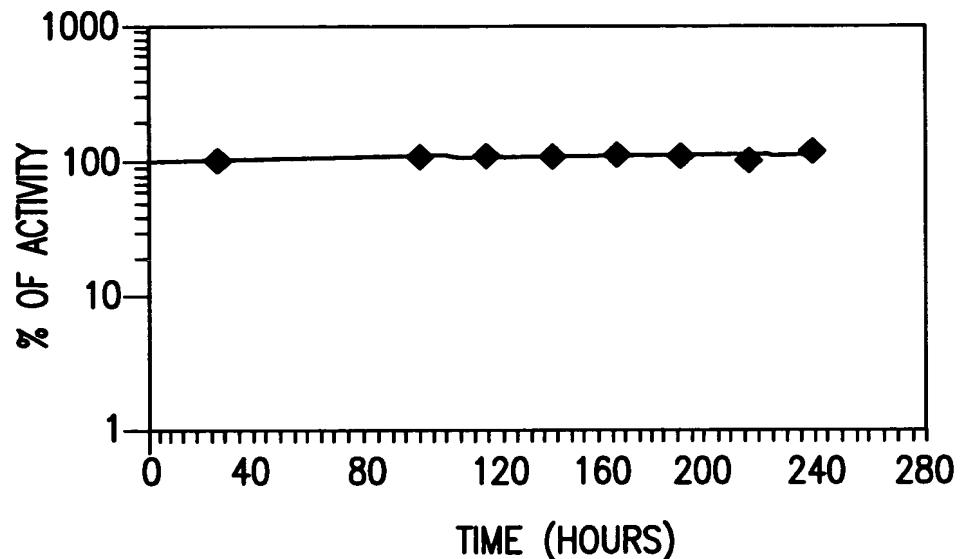


FIG.5

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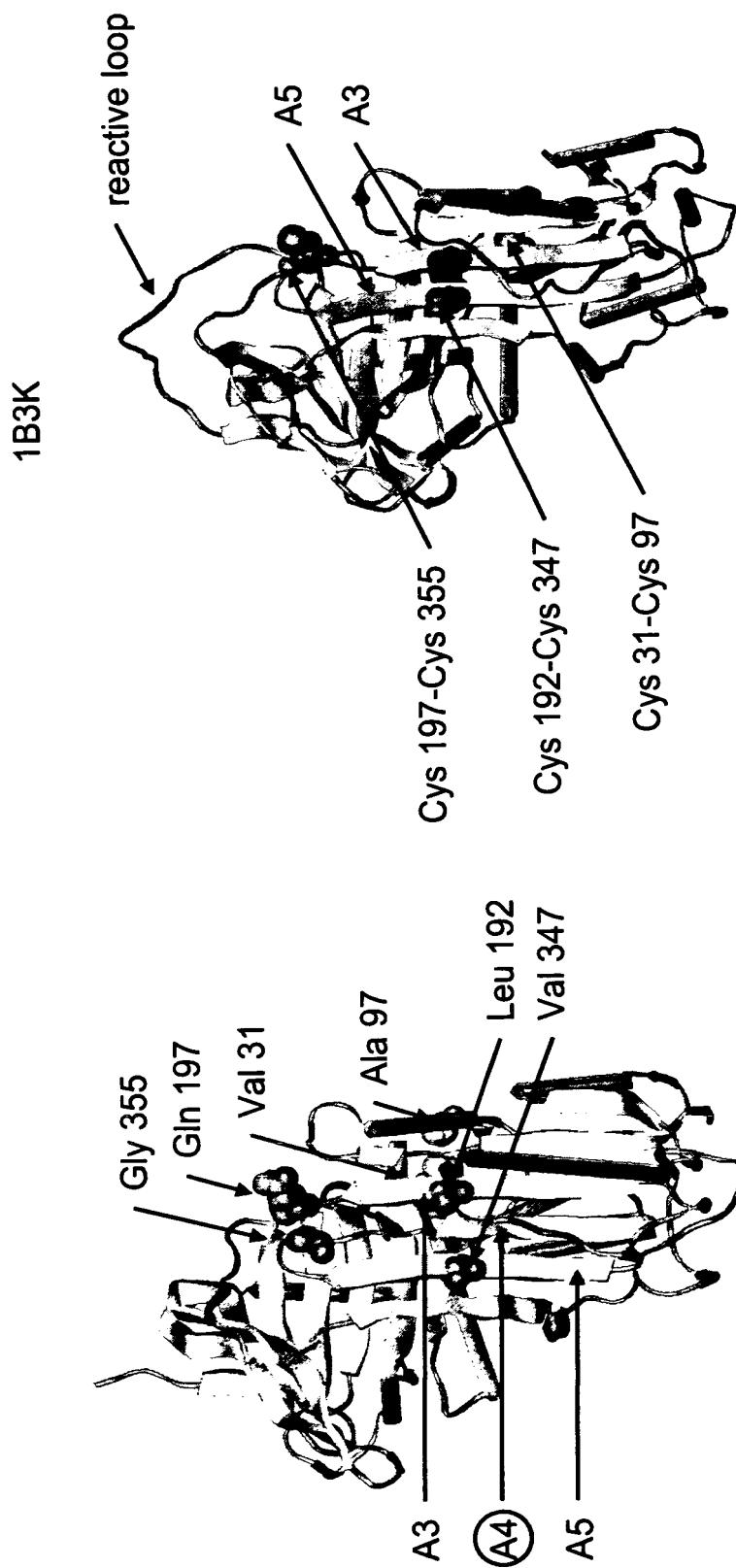


FIG. 6A

FIG. 6B

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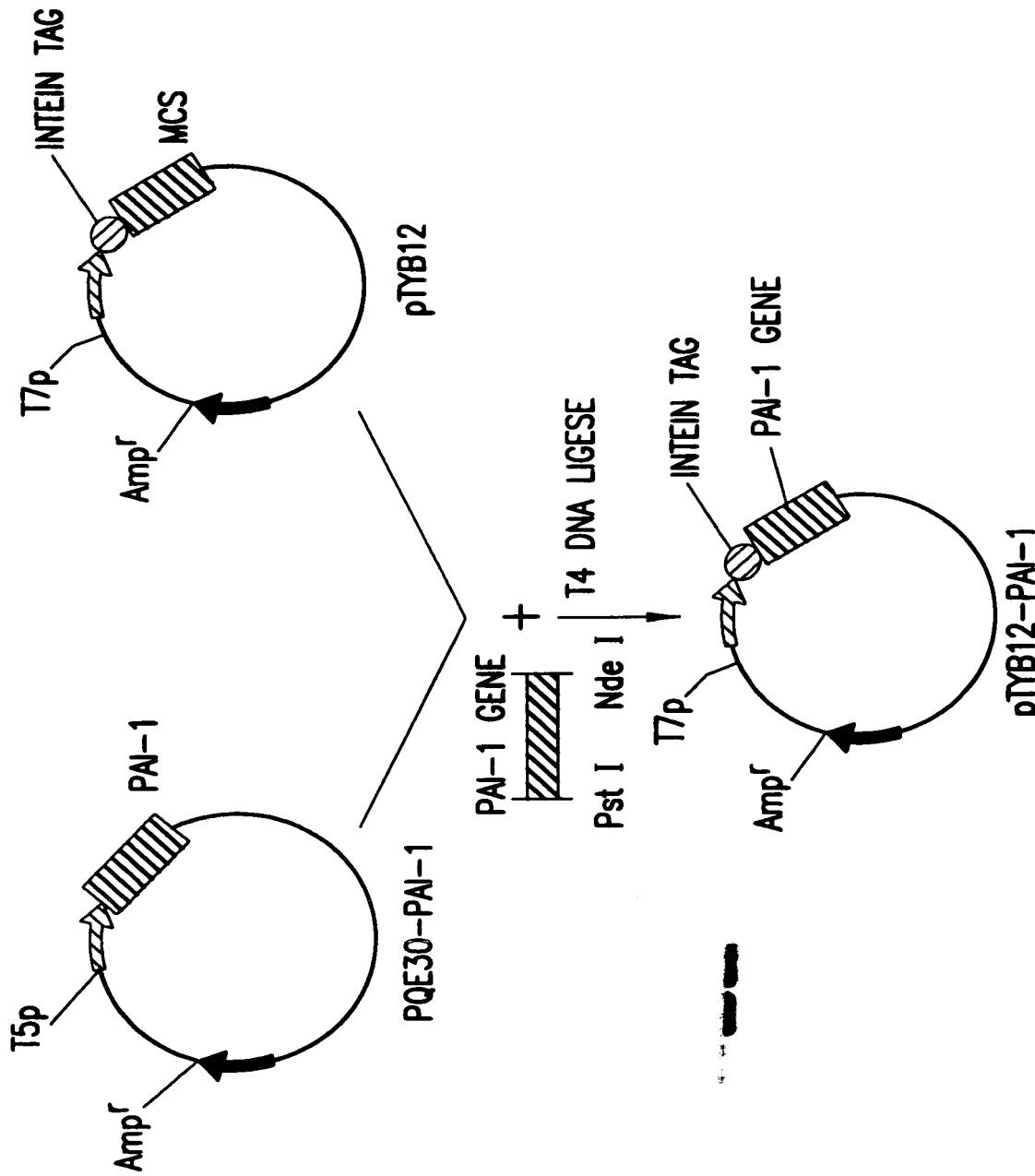


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FIG.8A

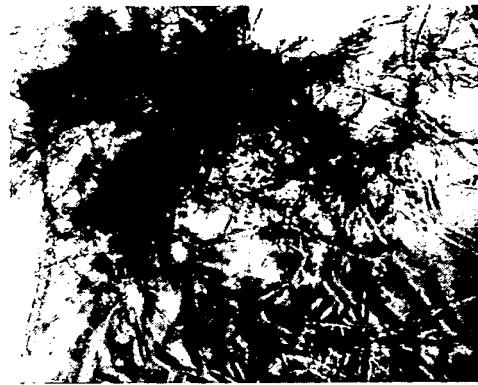


FIG.8B

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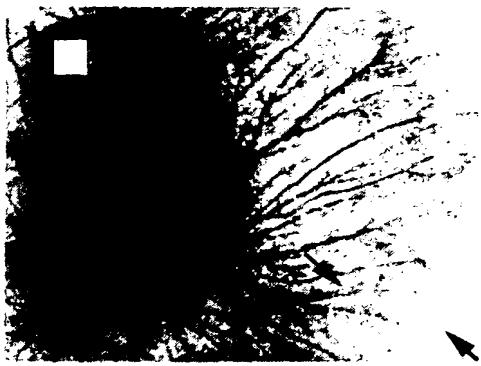


FIG. 9A



FIG. 9B

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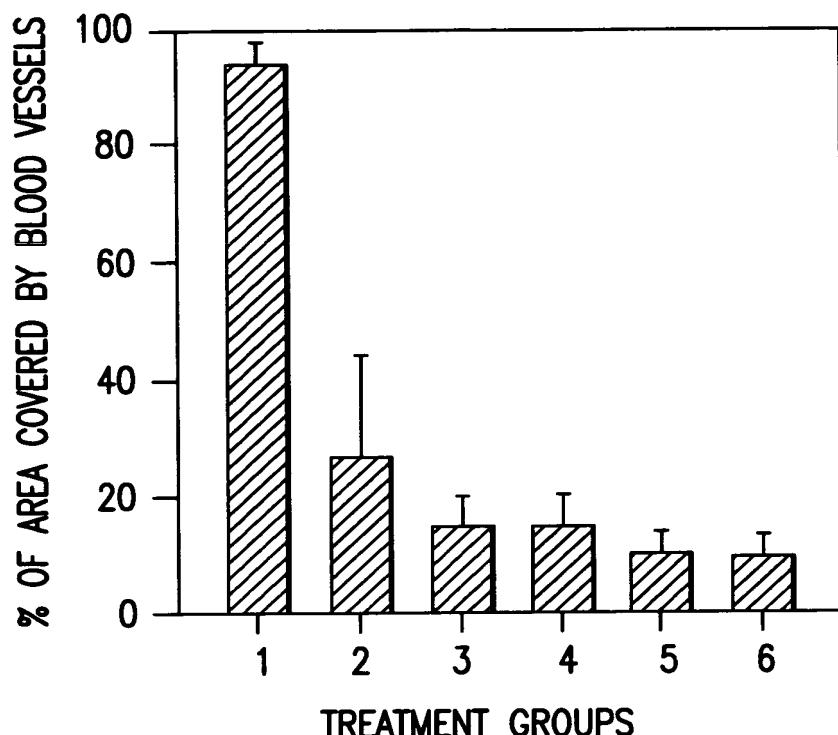


FIG. 10

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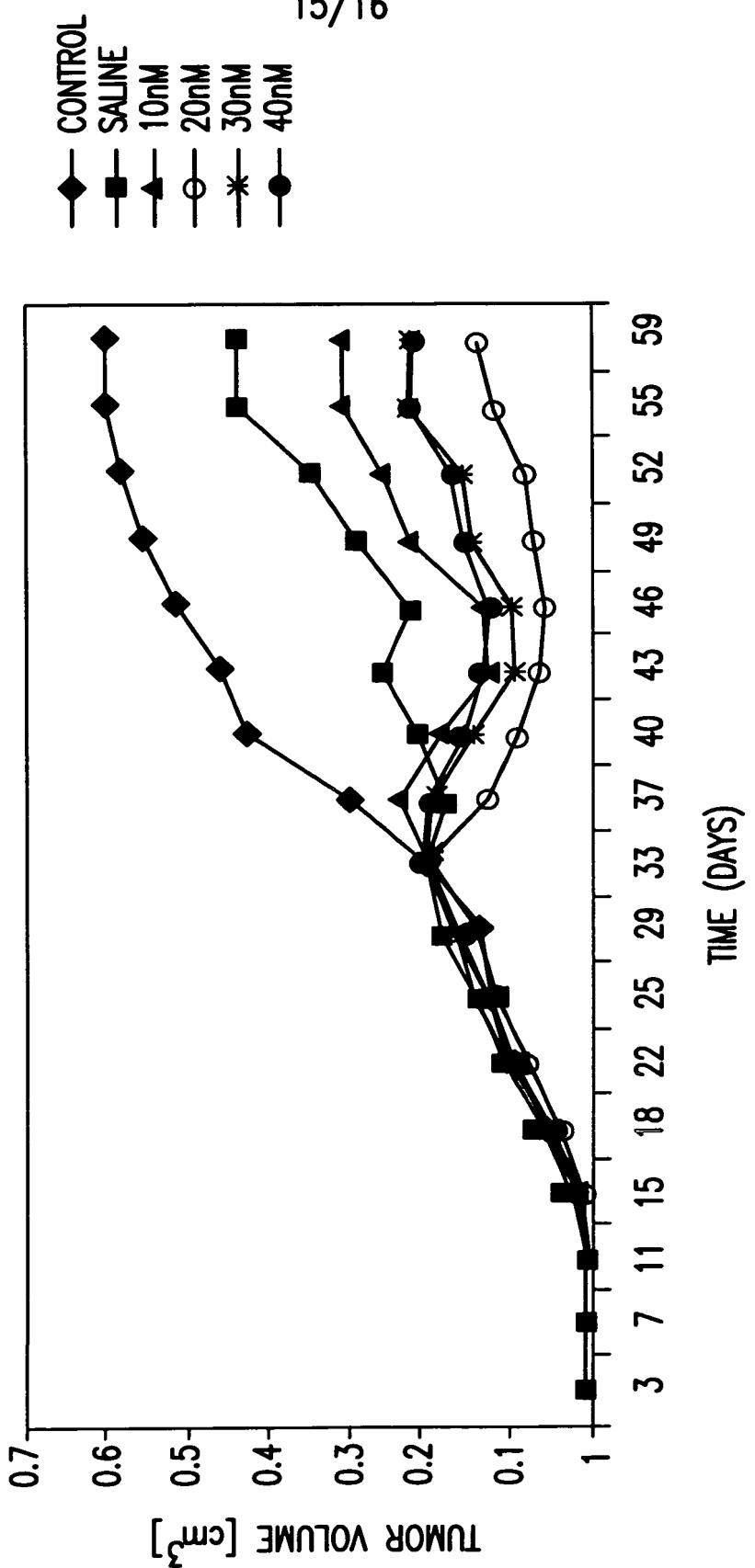


FIG. 11

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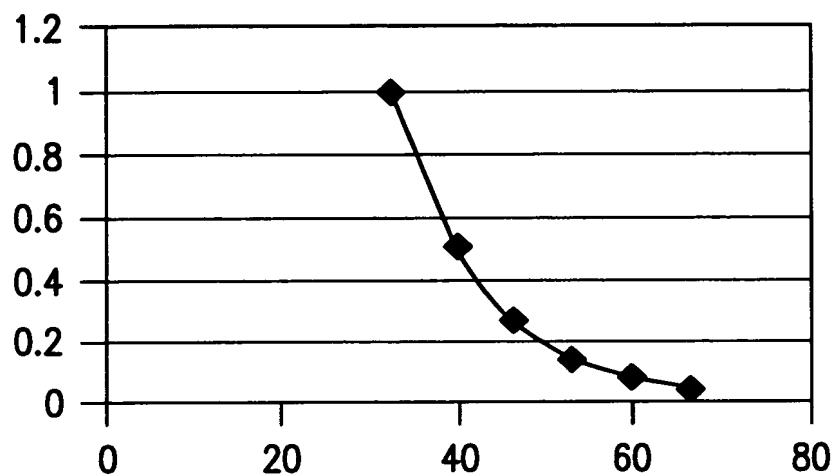


FIG. 12